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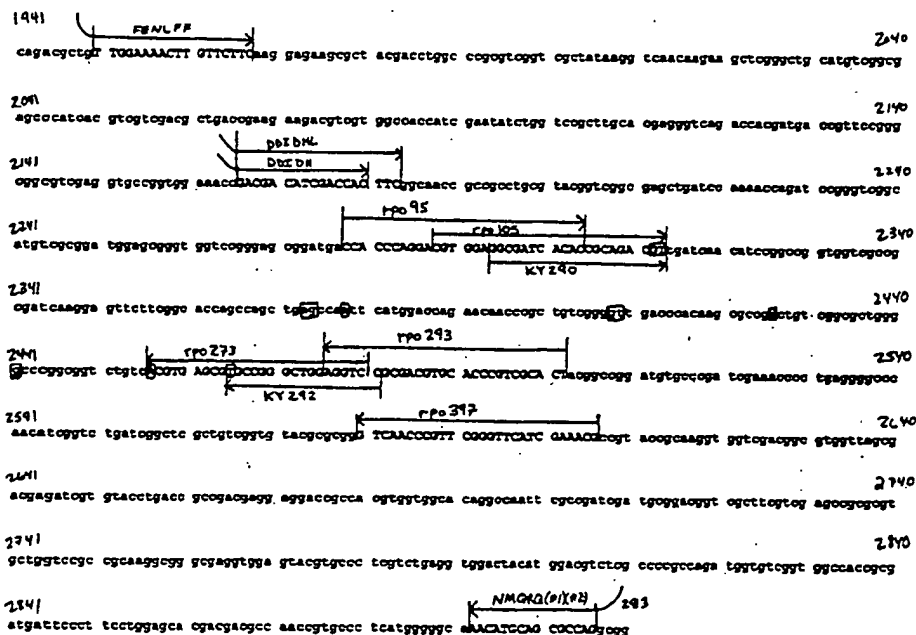
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(54) Title: DETECTION OF A GENETIC LOCUS ENCODING RESISTANCE TO RIFAMPIN



## (57) Abstract

A method is provided for detecting *M. tuberculosis* or mutants thereof, particularly rifampin-resistant MTB, in a biological sample comprising: isolating DNA from the biological sample; amplifying the isolated DNA under hybridizing conditions with a primer set that targets portions of the gene encoding rpoB; wherein the primer set comprises at least one primer that hybridizes under hybridizing conditions to at least one signature nucleotide for *M. tuberculosis*; and isolating and sequencing the amplified DNA to determine the presence or absence of *M. tuberculosis* or mutants thereof.

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DETECTION OF A GENETIC LOCUS ENCODING  
RESISTANCE TO RIFAMPIN

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Background of the Invention

After years of declining case rates, tuberculosis is again a major public health threat in the United States. Serious outbreaks involving patients infected with the human immunodeficiency virus (HIV) have occurred in several major metropolitan areas. Cases have also increased in other population groups, including the homeless, prisoners, migrant farm workers, immigrants, and health care workers.

Tuberculosis (TB) is a bacterial disease caused by organisms of the *M. tuberculosis* complex (i.e., *M. tuberculosis* (MTB), *M. bovis* and *M. africanum*). It is transmitted primarily by airborne droplets produced when individuals with pulmonary or laryngeal tuberculosis sneeze, cough, or speak. In the United States, the number of tuberculosis cases reported annually declined steadily between 1953 and 1985; however, in 1986 the rate for newly diagnosed cases began to increase, with a total of 26,283 cases were reported in 1991.

The antibiotic rifampin has long been an extremely effective antimicrobial agent and is one of the two major first-line anti-tuberculosis drugs. Rifampin has a unique site of action on the beta subunit (rpoB) of prokaryotic RNA polymerase, documented both biochemically (M.E. Levin et al., Molec. Microbiol., **8**, 277-285 (1993); F.G. Winder in The Biology of the Mycobacterial, Vol. 1, C. Ratledge et al., Eds., Academic Press: New York, pp. 353-438 (1982); and T. Yamada et al., Antimicrob. Agents Chemother., **27**, 921-924 (1985)), and genetically (D.J. Jin et al., J. Molec. Biol., **202**, 45-58 (1988); and N. Honoré et al., Antimicrob. Agents Chemother., **37**, 414-418 (1993)). Single site mutations in the gene for the beta subunit of RNA polymerase, *rpoB*, that confer rifampin resistance in *Escherichia coli* are well-characterized (Jin et al., J. Mol. Biol., **202**, 45-48 (1988)). Mutations conferring rifampin resistance in *M. tuberculosis* (Telenti et al., Lancet, **341**, 647-650 (1993)), *Mycobacterium leprae* (Honoré et al., Antimicrob. Agents Chemother., **37**, 414-418 (1993)), and *Mycobacterium smegmatis* (Levin et

al., Mol. Microbiol., 8, 277-285 (1993)) have been similarly mapped to the same region in the sequence encoding the beta subunit of RNA polymerase. The ability of single base-pair mutations in the *rpoB* region to confer rapidly developing high-level resistance to rifampin in *E. coli* is  
5 consistent with the known high frequency of developing rifampin resistance in MTB (M. Tsukamura, Tubercle, 53, 111-117 (1972)). The increasing incidence of rifampin-resistant MTB strains make it imperative to determine clinical drug susceptibility immediately upon diagnosis of TB.

Since 1990, outbreaks of multi-drug resistant tuberculosis  
10 (MDR-TB) involving over 200 patients have been reported to the Centers for Disease Control (CDC). All these outbreaks were characterized by the transmission of strains of *M. tuberculosis* resistant to at least isoniazid and rifampin, with some strains showing additional resistance to other drugs including ethambutol, streptomycin, ethionamide, kanamycin, and rifabutin.  
15 As used herein, MDR-MTB refers the the multi-drug resistant strains of the organism, *M. tuberculosis*, and MDR-TB refers to the drug-resistant disease produced by the multi-drug resistant organism. Delays in the laboratory diagnosis and reporting of drug-resistant tuberculosis contributed to the magnitude of these outbreaks since cases were not rapidly identified, the  
20 organism was not isolated, or the patients were not put on adequate therapy.

A conclusive diagnosis of tuberculosis depends on the isolation and identification of the etiologic agent, *Mycobacterium tuberculosis*, which generally requires 3-8 weeks. Design of an appropriate  
25 therapeutic regimen depends on the results of subsequent antituberculosis susceptibility testing by the agar dilution method and produces additional delays of 3-6 weeks (Roberts et al., "Mycobacterium" in Manual of Clinical Microbiology, 5th Ed.; A. Balows et al., Eds.; American Society for Microbiology: Washington; pp. 304-339 (1991). Identification and drug  
30 resistance testing can now also be accomplished more quickly by using the BACTEC radiometric method. (Tenover et al., J. Clin. Microbiol., 31, 767-779 (1993) and Huebner et al., J. Clin. Microbiol., 31, 771-775 (1993)). Acid fast bacilli are detected in the BACTEC bottle, and an identification is made using a nucleic acid hybridization technique on the BACTEC-derived growth.  
35 Drug susceptibility testing is then conducted using the same BACTEC

growth to inoculate fresh BACTEC bottles containing various antituberculous drugs. This procedure reduces the time needed to generate a complete analysis, but the total time required to report susceptibility results for MTB is still typically in excess of 20 days. The need to minimize the transmission of newly identified multi-drug resistant strains of MTB requires the development of much more rapid identification procedures.

Since rifampin resistance in MTB correlates well with multi-drug resistance (Fischl et al., Ann. Intern. Med., 117, 177-183 (1992); Frieden et al., N. Engl. J. Med., 328, 521-526 (1993); Goble et al., N. Engl. J. Med., 328, 527-532 (1993)), it can be used as a surrogate marker for MDR-MTB. Genotypic detection of multi-drug resistant MTB directly from clinical specimens is theoretically the fastest and most direct step toward determining effective therapy for patients infected with MDR-TB. A rapid test that could be performed directly on a patient specimen and that would both confirm a TB diagnosis and indicate whether it is a drug-resistant or drug-sensitive strain would be a major advance.

### Summary of the Invention

The present invention is directed to methods based on the polymerase chain reaction (PCR) for the detection of *Mycobacterium tuberculosis* (MTB) and concurrent determination of its drug susceptibility, utilizing the appropriate oligonucleotide primers. The methods are applicable to a wide variety of clinical and cultured specimens, and identify both resistant and non-resistant strains of MTB. The dual utility of the *rpoB* locus for both drug susceptibility and pathogen identification (MTB) may serve as a model for future rapid diagnostic methods development.

This invention involves a comparative analysis of the *rpoB* sequences in MTB, other mycobacteria and related GC-rich bacteria (Figure 1) demonstrating the heretofore undiscovered presence of a set of MTB-specific "signature nucleotides" that permits unequivocal identification of MTB strains, both drug-resistant and drug-sensitive. Utilization of this information in connection with sequencing the appropriate region on the *rpoB* gene can yield a positive identification of MTB along with essential information about its drug resistance phenotype. This invention therefore further relates to the use in polymerase chain reactions (PCR) of particular

oligonucleotide primers (Table 2) of varying levels of specificity: degenerate primers for all bacterial *rpoB* gene sequences; intermediate specificity primers for mycobacterial *rpoB* genes and *rpoB* genes from other GC-rich bacteria; and high specificity primers specific for the MTB *rpoB* gene. This invention also relates to the use of PCR and methods such as automated DNA sequencing, reverse dot blotting, microtitre plate oligonucleotide capture, single stranded conformational polymorphisms, dideoxy fingerprinting, and the like, to identify MTB and predict rifampin susceptibility directly from clinical specimens.

Accordingly, this invention provides a rapid, sensitive and specific process for detecting in vitro the presence of *Mycobacterium tuberculosis* and its drug-resistance phenotype. In accordance with the invention, the identification of *M. tuberculosis* involves the detection of all or some signature nucleotides in the *rpoB* gene of *mycobacterium tuberculosis*. The invention provides for the determination of rifampin resistance by detection of mutations in the *rpoB* gene of *M. tuberculosis*, particularly with respect to the nucleotide sequence of that same *rpoB* gene in mycobacterium tuberculosis that are not resistant to rifampin. Rifampin resistance is correlated with resistance to other drugs, thus this invention provides a means of detecting multi-drug resistant *M. tuberculosis*.

The invention utilizes polymerase chain reaction (PCR) to effect the determination of *M. tuberculosis* identity and drug susceptibility phenotype. This process comprises steps of isolation and purification of target DNA from bacterial cultures with clinical samples, and amplifying regions of the *rpoB* gene using specific oligonucleotide primers described herein. Amplified DNA is isolated and processed such that the sequence of nucleotides is determined. Inspection of the nucleotide sequence yields the useful information concerning organism identity and drug-susceptibility phenotype.

The PCR-based methods of the present invention are direct methods for the detection of *M. tuberculosis* DNA in a variety of biological samples, particularly human biological samples, e.g., fluid samples and tissue samples. The methods of the present invention are particularly advantageous because they have proven clinical value. That is, they show

greater than 90% sensitivity and greater than 90% specificity, and often greater than 95% sensitivity and 100% specificity.

One method of the present invention for detecting *M. tuberculosis* in a biological sample using PCR includes the steps of:  
5 isolating DNA from the biological sample; amplifying the isolated DNA under hybridizing conditions with a primer set that targets portions of the gene encoding *rpoB*; wherein the primer set comprises at least one primer that hybridizes under hybridizing conditions to a nucleotide sequence containing at least one signature nucleotide for *M. tuberculosis*; and isolating and  
10 analyzing the amplified DNA to determine the presence of *M. tuberculosis*, specific signature sequences, or significant mutations. Preferably, the method detects *M. tuberculosis* that is resistant to rifampin. More preferably, the method detects *M. tuberculosis* that is resistant to rifampin and at least one other antibiotic, i.e., multi-drug resistant-MTB.

15 The methods of the present invention use standard PCR techniques, preferably including single-tube hemi-nesting procedures as described herein for improving sensitivity and specificity. The primer sets used include at least one primer that hybridizes to a nucleotide sequence containing at least one signature nucleotide for *M. tuberculosis*, eleven of  
20 which are shown herein (Figure 2). Preferably, the signature nucleotide is contained within 5 nucleotides of the 3' end of the primer. More preferably, the signature nucleotide is the last nucleotide at the 3' end of the primer. Most preferably, such primers substantially correspond to a primer selected from the group consisting of *rpo105*, *rpo273*, *KY290*, and *KY292*, the  
25 sequences of which are shown in Table 2. Of these, *rpo105* and *rpo273* are the most highly specific for the MTB *rpoB* gene, and are therefore particularly preferred in the methods of the present invention. As used herein, "substantially corresponding to" means that the primer sequence of interest has at least about 50%, preferably at least about 80%, sequence identity  
30 with the referenced primer sequence. The PCR method preferably includes

amplification by a primer that is less specific than primers *rpo105*, *rpo273*, *ky290*, and *ky292*. These include primers that substantially correspond to a primer selected from the group consisting of *rpo95*, *rpo293*, and *rpo397*, the sequences of which are shown in Table 2. It should be noted that these  
5 sequences of intermediate specificity have a restriction site and 2-4 miscellaneous bases at the 5' end that do not necessarily hybridize to the *rpoB* gene.

Additionally, if desired, even less specific primers can be used in the method of the present invention. These primers are derived from an  
10 AT-rich portion of the bacterial gene encoding *rpoB*. This AT-rich portion encodes a highly conserved amino acid sequence. Preferably, these primers hybridize to the *rpoB* gene in regions delineated by nucleotides 1945-1980, 2155-2190, and 2885-2910, as shown in Figure 3. As used  
15 herein, "highly conserved" means that these portions of the amino acid sequence have at least about 75% sequence identity among all species analyzed to date.

All primers used in the methods of the present invention have at least 14 nucleotides, preferably about 14-75, more preferably about 14-50, and most preferably about 15-30 nucleotides. The hybridizing and  
20 amplification conditions used in the present invention include an annealing temperature of about 60-75°C, an extension temperature of about 70-90°C, and a denaturation temperature of about 90-100°C for a total of about 30-50 cycles in a PCR mix containing a sufficient amount of buffer to maintain the pH at 8-8.5, and a sufficient amount of each of the following reagents to  
25 maintain: a final concentration of 50-200 micromolar or each dNTP; a final concentration of 0.1-2 micromolar primer; a final volume-% of 5-15% glycerol; and about 0.1-1 Unit of AmpliTaq per 50 microliters of the total volume of the reaction mixture.

### 30 Brief Description of the Drawings

Figure 1. Alignment of a portion of amino acid sequences for the beta subunit of RNA polymerase (*rpoB*) from *Mycobacterium leprae*,



*Mycobacterium tuberculosis*, *Escherichia coli*, *S. typhimurium* and *P. putida*. Underlined residues (FENLFF, DDIDHL and NMQRQ) indicate regions that are highly conserved within the bacterial kingdom and that were used in the development of the degenerate primers listed in Table 2. The numbering system is arbitrary and assigned by the GCG software.

Figure 2. Alignment of a portion of *rpoB* DNA sequences from *M. tuberculosis* and other GC-rich bacteria. Base numbering system is that of L.P. Miller et al. for the entire 3533 base pair *rpoB* gene, GenBank accession number L27989 (1994). Lower-case nucleotides indicate those differing from the consensus sequence. A dot (.) indicates that there was no DNA sequence to be read at that position. The letter (N) in the consensus sequence indicates that the automated sequencer could not identify the base at that position, and a hyphen (-) indicates a gap in the sequence. Positions of MTB "signature nucleotides" at base numbers 2312-2313 (129-130), 2373-2374 (190-191), 2378 (195), 2408-2409 (225-226), 2426 (243), 2441 (258), 2456 (273) and 2465 (282), are indicated at the top of the figure by an asterisk (\*). Numbers in parenthesis are the corresponding base pair numbers according to the numbering system of Telenti et al., Lancet, 34, 647-650 (1993), Genbank Accession Number L05910. For those strains having several different entries in the figure, each entry represents a distinct patient sample.

Figure 3. A diagram and partial nucleotide sequence of the *rpoB* gene from *M. tuberculosis*. Location of hybridization of oligonucleotide primers described in Table 2 is indicated by arrows and capitalized portions of the sequence. Boxed nucleotides indicate *M. tuberculosis* signature nucleotides described in Table 5.

### Detailed Description of the Invention

Polymerase chain reaction (PCR), an extremely rapid and sensitive method of detecting and amplifying DNA, is finding increasing use in genotypic detection of drug resistance as mechanisms of drug resistance become elucidated (Finken et al., Molecular Microbiol., 9, 1239-1246, (1993); J.J. Goswitz et al., Antimicrob. Agents Chemother., 36, 1166-1169 (1992); Y. Zhang et al., Nature, 358, 591-593 (1992)). It forms the basis of the method of the present invention for direct detection of *M. tuberculosis* and its drug susceptibility.

Rifampin is a bacterial drug which is particularly potent against the tuberculosis group of mycobacteria - *Mycobacterium tuberculosis*, *M. bovis*, and *M. africanum* - and, in consequence, it has been particularly effective in the treatment of tuberculosis. Standard anti-tuberculosis regimens generally include INH rifampin, or isoniazid, often in combination with the weaker drugs pyrazinamide, ethambutol, or streptomycin. Besides its use in therapy, rifampin is also given to close contacts of patients as a prophylactic measure.

The sequences of the *rpoB* genes for various organisms that are included in the alignment were derived by standard sequence techniques. The base sequences of the nucleotides are written in the 5' → 3' direction. Each of the letters shown is a conventional designation for the following nucleotides: A - Adenine; G - Guanine; T - Thymine; and C - Cytosine. The oligonucleotide primer sequences included as part of the invention can be prepared by the formation of 3' → 5' phosphate linkages between nucleoside units using conventional chemical synthesis techniques. For example, the well-known phosphodiester, phosphotriester, and phosphite triester techniques, as well as known modifications of these approaches, can be employed. Deoxyribonucleotides can be prepared with automatic synthesis machines, such as those based on the phosphoramidite approach. Oligo- and polyribonucleotides can also be obtained with the aid of RNA ligase using conventional techniques.

The nucleotide sequences of the invention are in a purified form. For instance, the nucleotides are free of human blood-derived proteins, human serum proteins, viral proteins, nucleotide sequences encoding these proteins, human tissue, and human tissue components. In

addition, it is preferred that the nucleotides are free of other nucleic acids, extraneous proteins and lipids, and adventitious microorganisms, such as bacteria and viruses.

5 This invention includes variants of the nucleotide sequences of the invention exhibiting the same selective hybridization properties as the oligonucleotide primers identified herein. The nucleotide sequences of the present invention can be employed in PCR which is advantageous because this technique is rapid and sensitive.

10 DNA primer pairs of known sequence positioned 10-300 base pairs apart that are complementary to the plus and minus strands of the DNA to be amplified can be prepared by well known techniques for the synthesis of oligonucleotides. One end of each primer can be extended and modified to create restriction endonuclease sites when the primer is annealed to the target DNA. The PCR reaction mixture can contain the  
15 target DNA, the DNA primer pairs, four deoxyribonucleoside triphosphates,  $MgCl_2$ , DNA polymerase, and conventional buffers. The DNA can be amplified for a number of cycles. It is generally possible to increase the sensitivity of detection by using a multiplicity of cycles, each cycle consisting of a short period of denaturation of the target DNA at an elevated  
20 temperature, cooling of the reaction mixture, and polymerization with the DNA polymerase.

Single-strand conformation polymorphism (SSCP) analysis can be used to detect DNA polymorphisms and point mutations in a variety of positions in amplified DNA fragments. Alternatively, a portion of the PCR  
25 reaction mixture can be separated and subjected to hybridization with an end-labeled nucleotide probe, such as a  $^{32}P$  labeled adenosine triphosphate end-labeled probe. The amplified product can be isolated and sequenced to obtain information at the nucleotide level.

Since it may be possible to increase the sensitivity of detection  
30 by using RNA instead of chromosomal DNA as the original template, this invention contemplates using RNA sequences that are complementary to the DNA sequences described herein. The RNA can be converted to complementary DNA with reverse transcriptase and then subjected to DNA amplification.

The following examples are offered to further illustrate the various specific and preferred embodiments and techniques. It should be understood, however, that many variations and modifications may be made while remaining within the spirit and scope of the present invention.

## EXPERIMENTAL EXAMPLES

Example 1.Correlation of Rifampin Resistance with Multi-drug  
Resistance in *M. tuberculosis*

5

TABLE 1

Rifampin resistance patterns among 83 drug-resistant  
*M. tuberculosis* isolates from 1/1/90-12/31/92,  
Mayo Clinic Mycobacteriology Laboratory (Total n = 787).

<u>Resistance<sup>1</sup>-to:</u>	<u>Rifampin resistant / Total resistant</u>	<u>Percent</u>
1 drug	7/54	13
2 drugs	3/10	30
3 drugs	8/9	89
4 drugs	4/5	80
5 drugs	5/5	100

<sup>1</sup> Resistance is defined as growth of more than 1% of a ca. 200-cfu inoculum after 2 wk incubation at 35°C in air on Middlebrook 7H11 agar containing one of the following drugs (concentrations, µg/mL, in parentheses): Isoniazid (4), rifampin (4), streptomycin (16), ethambutol (8), pyrazinamide (32) (Dimed Inc., St. Paul, MN).

10

Example 2.Detection of Rifampin Resistance in Mycobacterial Cultures and  
Clinical Specimens using Oligonucleotide PrimersDDIDHL, NMQRQ, rpo95, rpo293 and rpo397

15

Oligonucleotide primers DDIDHL, NMQRQ(#1), rpo95, rpo293 and rpo397 (Table 2) were used to amplify *rpoB* deoxyribonucleic acid (DNA) from bacterial cultures and clinical isolates using the methods and producing the results described below.

20

TABLE 2		
LIST OF PRIMERS		
Primer Name	Sequence	Length
DDIDHL <sup>1</sup>	5' TTG AAT TCG A(CT)G A(CT)A T(CT)G A(CT)C A(CT)C T 3'	25-mer
DDIDHL <sup>2</sup>	5' GTC CCT GCA GGA CGA CAT CGA CCA C 3'	25-mer
NMQRQ (#1) <sup>3</sup>	5' TTG GAT CC(CT) TG(AGC) CG(CT) TGC AT(AG) TT 3'	23-mer
NMQRQ (#2) <sup>4</sup>	5' GGG ATC CGC (TC)TG CG(CT) TGC ATG TT 3'	23-m34
FENLFF <sup>5</sup>	5' CCC TGC AGT TCG AGA ACC TGT TCT TC 3'	26-mer
rpo95	5' CCA CCC AGG ACG TGG AGG CGA TCA CAC 3'	27-mer
rpo293	5' AGT GCG ACG GGT GCA CGT CGC GGA CCT 3'	27-mer
rpo397	5' CGT TTC GAT GAA CCC GAA CGG GTT GAC 3'	27-mer
rpo105	5' CGT GGA GGC GAT CAC ACC GCA GAC GT 3'	26-mer
rpo273	5' GAC CTC CAG CCC GGC ACG CTC ACG T 3'	25-mer
KY290	5' GGC GAT CAC ACC GCA GAC GT 3'	20-mer
KY292	5' GGA CCT CCA GCC CGG CA 3'	17-mer

<sup>1</sup> The first eight bases comprise a nonhybridizing tail consisting of two (TT) filler bases followed by GAATTC, a restriction site for *EcoR*1 restriction enzyme incorporated to facilitate cloning using the amplicon at a later date, if desired. The remaining bases hybridize to bacterial *rpoB* DNA

<sup>2</sup> The first ten bases comprise a nonhybridizing tail consisting of four filler bases (GTCC) followed by CTGCAG, a restriction site for *pst*1 restriction enzyme incorporated to facilitate cloning using the amplicon at a later date, if desired. The remaining bases hybridize to bacterial *rpoB* DNA.

<sup>3</sup> The first several bases comprise a nonhybridizing tail consisting of filler bases followed by a restriction site for incorporated to facilitate cloning using the amplicon at a later date, if desired. The remaining bases hybridize to bacterial *rpoB* DNA.

4 The first several bases comprise a nonhybridizing tail consisting of filler  
bases and a restriction site to facilitate cloning using the amplicon at a  
later date, if desired. The remaining bases hybridize to bacterial *rpoB*  
5 DNA.

5 The first eight bases comprise a nonhybridizing tail consisting of two filler  
bases (CC) followed by CTGCAG, a restriction site for *psfI*; restriction  
enzyme incorporated to facilitate cloning using the amplicon at a later  
10 date, if desired. The remaining bases hybridize to bacterial *rpoB* DNA.

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A. Clinical isolates and reference strains. Reference strains  
15 (Table 3) were obtained from the American Type Culture Collection (ATCC)  
and propagated using standard laboratory methods. Clinical specimen  
sources for bacteria were isolated and identified as part of routine clinical  
laboratory processing of such specimens. Susceptibility to rifampin and  
other anti-mycobacterial antibiotics was determined by the 1% proportion  
20 method as defined by G.D. Roberts et al. Manual of Clinical Microbiology,  
5th Edition; A. Balows et al., Eds.; American Society for Microbiology:  
Washington, D.C.; pp. 304-339 (1991) (incorporated herein by reference).  
Resistance to rifampin was defined as >1% growth of a standard inoculum  
on Middlebrook 7H10 agar containing 4 µg/mL rifampin (Dimed, St. Paul,  
25 MN).

TABLE 3

Amplification of the *rpoB* locus from a panel of bacterial DNAs  
using PCR primers *rpo95* and *rpo293*

5		<u>Mycobacteria:</u>	<u><i>rpoB</i> Amplified</u>
		<i>M. avium</i> complex	yes
		<i>M. fortuitum</i>	yes
10		<i>M. marinum</i>	yes
		<i>M. phlei</i>	yes
		<i>M. smegmatis</i>	yes
		<i>M. triviale</i>	yes
		<i>M. tuberculosis</i>	yes
15		<i>M. xenopi</i>	no
		<u>Other GC-rich Bacteria:</u>	
		<i>Actinomyces</i> sp.	yes
		<i>Corynebacterium</i> sp.	yes
20		<i>Rhodococcus</i> sp.	yes
		<i>Streptomyces</i> sp.	yes
		<u>Other Bacteria:</u>	
		<i>Haemophilus influenzae</i>	no <sup>1</sup>
25		<i>Nisseria</i> sp. (3 isolates)	no
		<i>Staphylococcus</i> sp.	no
		<i>Streptococcus</i> sp. (6 isolates)	no
		<i>Peptostreptococcus</i> sp.	no
		<i>Veillonella</i> sp.	no
30		<i>Lactobacillus</i> sp.	no

<sup>1</sup> The first isolate tested was probe-positive, but a second isolate was negative. The initial result was judged to be a false positive.



B. Bacterial DNA isolation. DNA from cultured isolates of bacteria and mycobacteria was prepared for polymerase chain reaction (PCR) amplification by either the bead-beat/boil (BB/B) method or by bead-beat/phenol (BB/P) extraction. For the BB/B method, a 10- $\mu$ L loopful of each isolate was harvested and placed in a 2.0-ml screw cap microcentrifuge tube (Sarstedt, Inc.) filled 2/3 full with 0.1 mm diameter zirconium beads (Biospec Products, Bartlesville, OK) and 1.0 mL lysis buffer (lysis buffer: 10 mM Tris(hydroxymethyl)aminomethane hydrochloride (Tris-HCl), pH 8.0, 1 mM ethylenediaminetetraacetic acid (EDTA), 1% Triton-X100 (all from Sigma Chemical Company, St. Louis, MO)). Tubes were oscillated on a Mini Bead Beater (Biospec Products, Bartlesville, OK) for 30 seconds. The supernatant was pipetted into a clean tube, boiled 30 minutes to kill the bacteria, and stored at -20°C. Two  $\mu$ L was used as PCR target in 50- $\mu$ L PCR reactions. For the BB/P extraction method, a 10- $\mu$ L loopful of the isolate was placed in a 300- $\mu$ L volume of phenol, equilibrated with TE buffer (TE buffer: 10 mM Tris-HCl, pH 8.0, 1 mM EDTA), in a 300- $\mu$ L screw cap microcentrifuge tube (Sarstedt, Inc.) 2/3 filled with 0.1-mm diameter zirconium beads, 150  $\mu$ L TE buffer was added, and the mixture was oscillated 30 seconds on a Mini Bead Beater. The tubes were incubated 30 minutes at 25°C to kill bacteria before being centrifuged for 20 seconds in a microcentrifuge to separate phases. The aqueous phases were pipetted into clean tubes and stored at -20°C. Purified DNA was extracted from the aqueous phases by using Isoquick nucleic acid extraction kit reagents (Microprobe, Garden Grove, CA 92641). Five  $\mu$ L of 1/10 or 1/100 dilutions of purified DNA in water was used as target in all PCR reactions.

C. DNA extraction from clinical specimens. Clinical specimens (respiratory: sputum, bronchial wash; non-respiratory: urine) were processed by 1% NaOH (Sigma Chemical Company, St. Louis, MO) liquefaction-decontamination and sedimentation, and 0.5 ml of sediments were inoculated into 7H10, Selective 7H11, and Bactec 12B media (see G.D. Roberts et al., "Mycobacterium", in Manual of Clinical Microbiology, 5th Edition; A. Balows et al., Eds.; American Society for Microbiology: Washington; pp. 304-339 (1991)). DNA was isolated from 1.0 ml of the residual sediment by centrifugation for 15 minutes in microcentrifuge tubes;

the supernatant was subsequently removed and discarded. Zirconium beads (0.1mm diameter) were added to 2/3 tube volume, and 600  $\mu$ L phenol plus 400  $\mu$ L TE buffer were added, and the screw-capped tube subjected to bead-beating for 30 seconds followed by a 15 minute incubation at 25°C to kill organisms, and 3 minutes centrifugation at 16000 x g in a microcentrifuge to separate the phases. The aqueous phase was transferred to clean tubes and stored at -20°C. DNA was further extracted from the aqueous phases by using the Isoquick DNA extraction kit. Five  $\mu$ L of 1/10 or 1/100 dilutions of purified DNA in water were used as target in PCR reactions.

D. Design of sequence degenerate primers DDIDHL and NMQRQ. Oligonucleotide primers DDIDHL and NMQRQ (Table 2) were designed to hybridize to portions of the *rpoB* gene that are highly conserved within the bacterial kingdom (Figure 1). The amino acid sequence alignment in Figure 1 was created using the Pileup utility of Genetics Computer Group (Madison, WI). DDIDHL is named for the highly conserved bacterial *rpoB* amino acid sequence aspartate(D)-aspartate(D)-isoleucine(I)-aspartate(D)-histidine(H)-leucine(L) (e.g. amino acids #442-448 in the *rpoB* protein from *M. tuberculosis*), and NMQRQ is named for the highly conserved amino acid sequence asparagine(N)-methionine(M)-glutamine(Q)-arginine(R)-glutamine(Q) (e.g. amino acids #684-688 in the *rpoB* protein from *M. tuberculosis*) (Figure 2). Degenerate nucleotides were chosen such that the same amino acid is encoded at every position (using different three-nucleotide codons). These regions were ideally suited to *rpoB*-specific priming because they contain AT-rich codons in a genome that is otherwise rich in GC base pairs. DDIDHL and NMQRQ were intended to amplify most bacterial *rpoB* gene sequences.

E. Polymerase chain reactions. Primers DDIDHL, NMQRQ, *rpo95*, *rpo293* and *rpo397* (Table 2) were synthesized on an ABI Model 394 Synthesizer (Applied Biosystems, Inc., Foster City, CA). PCR reactions (50  $\mu$ L) contained target DNA (5  $\mu$ L), 1  $\mu$ M primers, 10% glycerol (Sigma Chemical Company, St. Louis, MO), 2 mM  $MgCl_2$  (Sigma Chemical Company, St. Louis, MO), 0.2 mM each deoxyadenosine triphosphate (dATP), deoxyguanine triphosphate (dGTP), deoxycytidine triphosphate (dCTP), and deoxyuridine triphosphate (dUTP) (all nucleoside

triphosphatases (dNTPs) from Boehringer Mannheim Biochemicals, Indianapolis, IN), 1.25 unit AmpliTaq polymerase (Perkin-Elmer Cetus, Norwalk, CT), and 1X Perkin-Elmer Cetus PCR buffer II. Either a Temptronic Series 669 (Barnstead-Thermolyne, Dubuque, IA 52004) or  
5 Perkin-Elmer Cetus Model 9600 thermal cycler was used with identical cycling parameters. Amplification with DDIDHL (upstream) and NMQRQ (downstream) was accomplished using 40 cycles of 94°C (1 minute) and 55°C (1 minute), and 72°C (3 min), after an initial 4 minutes at 94°C to denature input DNA, with a final 5 minutes at 72°C for strand extension.  
10 Amplification with upstream primer rpo95 and either downstream primer rpo293 (producing a 224 base pair amplicon) or rpo397 (producing a 328 base pair amplicon) was done using 50 cycles of 94°C (1 minute) and 65°C (1 minute), after an initial 4 minute at 94°C to denature input DNA, with a final 4 minute at 72°C for strand extension. Amplification products were  
15 detected by agarose gel electrophoresis of 1/5 or 1/10 of the reaction mixture in 2% agarose (Seakem GTG, FMC, Rockland, ME) made up in 1X Tris-borate-EDTA (TBE) (0.089M Tris-borate, 0.089M boric acid, 2mM EDTA), followed by staining with ethidium bromide. The products were purified by using Magic PCR Prep kit reagents (Promega, Madison, WI),  
20 and sequenced by using primer rpo95 at the Mayo Clinic Molecular Biology Core Facility using an Applied Biosystems 373A automated sequencer and the dye-coupled dideoxyribonucleotide cycle sequencing method (Applied Biosystems Inc. Foster City, CA). Sequencing reactions were run using 5% (v/v) dimethylsulfoxide for twenty-five cycles of 96°C (30 seconds), 50°C (15  
25 seconds), 60°C (4 minutes). To provide additional detection sensitivity, Southern blots of agarose gels were prepared on nylon membranes (Nytran, #77593, Schleicher and Schuell, Keene NH) by overnight capillary blotting followed by UV-crosslinking. The blots were probed with a 328-bp MTB *rpoB* amplification product of primers rpo95 and rpo397 which was directly  
30 coupled with horseradish peroxidase using ECL kit reagents according to the manufacturer's recommendations (Amersham, Arlington Heights, IL). Hybridization conditions (42°C, 16 hours) specified by the kit manufacturer were used. Chemiluminescence was detected by exposure of Kodak AR X-ray film for 5 minutes.

F. PCR Results. A PCR product of the expected size, ca. 700 base pair, was obtained after amplification of genomic target DNA extracted from *E. coli* and two MTB isolates, one resistant and one susceptible to rifampin. The more specific primers *rpo95*, *rpo293* and *rpo397* amplified reference mycobacterial *rpoB* gene sequences, including both resistant and non-resistant MTB but excluding *M. xenopi*, and *rpoB* DNA from other GC-rich organisms, but not *rpoB* from other bacteria (Table 3). Clinical results, reported in Table 4 showed that identification and drug susceptibility phenotype obtained directly by sequencing the PCR product confirmed the results of acid-fast testing, culture, and actual drug susceptibility testing.

**TABLE 4**Summary of *rhoB* PCR results with 16 clinical specimens

Specimen	Source	Acid-fast Smear <sup>1</sup>	Culture <sup>2</sup>	Signature Sequence <sup>3</sup>	Rifampin Phenotype of Isolate	
					Predicted <sup>4</sup>	Actual <sup>5</sup>
1	Sputum	+	MTB	MTB	Rif-S	Rif-S
2	Sputum	-	-	-		
3	Sputum	+?	-	Ambiguous		
4	Sputum	-	-	-		
5	Urine	-	-	-		
6	Sputum	+	MAC	Ambiguous		
7	Sputum	-	-	-		
8	Tr. Sec. <sup>6</sup>	-	-	-		
9	Br. Wash	-	MTB	-		
10	Sputum	-	-	-		
11	Sputum	+	MTB	MTB	Rif-S	Rif-S
12	Sputum	-	MAC	-		
13	Sputum	-	MTB	MTB	Rif-S	Rif-S
14	Sputum	-	-	-		
15	Sputum	-	MTB	MTB	Rif-S	Rif-S
16	Sputum	+	MTB	MTB	Rif-R	Rif-R

<sup>1</sup> Smears stained with auramine-rhodamine (Truant's) reagents and screened microscopically at 250X. Quantitation is Negative (0/smeas), Positive rare (3-9/smeas), Positive few (>10/smeas), or Positive many (>1/microscope field).

- <sup>2</sup> Negative culture results means no growth after 60 days. MAC is *Mycobacteria avium-intracellulare*
  - <sup>3</sup> Amplification products were sequenced only if a signal was seen on a Southern blot. Identification of MTB was based on occurrence of specific MTB-specific signature sequences at positions indicated in Example 3 (Table 5). A (-) indicates that no PCR product was detected after amplification. Amplification was done with rpo95 upstream and rpo293 (for specimen nos. 1-12) or rpo397 (for specimen nos. 13-16) downstream.
  - <sup>4</sup> Prediction of rifampin phenotype as sensitive (Rif-S) or resistant (Rif-R) was based on analysis of amplified rpoB DNA sequences directly from the clinical specimens.
  - <sup>5</sup> Susceptibility determined by agar dilution. The MDR-MTB isolate from specimen no. 16 was resistant to cycloserine, ethambutol, pyrazinamide, and rifampin.
  - <sup>6</sup> Tracheal secretions.
-

Example 3.Identification of MTB signature nucleotides

DNA sequences obtained through the use of the rpo95/rpo293 and rpo95/rpo397 primer pairs described in Example 2 were aligned using the GCG nucleic acid analysis software (Genetics Computer Group, Madison WI) running on a VAX computer in the Mayo Clinic/Foundation Research Computing Facility (Figure 2). Nucleotides were numbered with reference to the 432-bp *M. tuberculosis* rpoB region sequenced by Telente et al., Lancet, 341, 647-650 (1993) (incorporated herein by reference). The GCG Pileup utility was used to generate the sequence alignments, using default parameters when options were available. The results of the Pileup analyses were used as input for the GCG Pretty utility. Pretty generated a consensus sequence and displayed only nucleotides that differed from the consensus strand. It was found upon inspection of the sequence alignment that there were eleven sites (positions 129-130, 190-191, 195, 225-226, 243, 258, 273 and 282) at which the nucleotide observed for *Mycobacterium tuberculosis* (MTB) differed from all or most related organisms (Table 5). A combination of all or some of these bases (the "signature" nucleotides, defined as G129, T130, A190, G191, A195, G225, T226, A243, G258, A273, and T282) was unique to MTB and common to 60+ MTB strains sequenced. This was true regardless of whether the MTB strain was resistant or sensitive to rifampin, as the mutations that lead to rifampin resistance occur at other locations. Telente et al., Lancet, 341, 647-650 (1993)

**TABLE 5****Signature nucleotides within the *rpoB* gene of *M. tuberculosis***

<b>Nucleotide<sup>1</sup> Position</b>	<b>MTB Signature<sup>2</sup></b>	<b>Exceptions (same base or base pair as MTB)<sup>3</sup></b>
129-130 (2312-2313)	gac GT tga	<i>M. bovis</i>
190-191 (2373-2374)	ctg AG cca	<i>Actinomyces sp.</i> , <i>M. aurum</i> , <i>M. bovis</i>
195 (2378)	cca A ttc	<i>M. bovis</i>
225-226 (2408-2409)	ggg GT tga	<i>M. triviale</i> , <i>M. bovis</i>
243 (2426)	ccg A ctg	<i>M. bovis</i>
258 (2441)	ggg G ccc	<i>M. triviale</i> , <i>M. marinum</i> , <i>M. kansasii</i> , <i>Nocardia sp.</i> , <i>propionibacter sp.</i> , <i>rhodococcus sp.</i>
273 (2456)	gtc A cgt	<i>M. bovis</i>
282 (2465)	gcg T gcc	<i>M. kansasii</i> , <i>M. bovis</i>

<sup>1</sup> Nucleotide numbering based on Telente et al., *Lancet*, 341, 647-650 (1993). Numbers in parentheses are based on the numbering system of L.P. Miller et al., for the entire *rpoB* gene sequence GenBank accession No. L27989.

<sup>2</sup> MTB signature bases (capital letters) are not altered in rifampin-resistant MTB.

<sup>3</sup> Differences in nucleotide sequence at other locations are also present.



Example 4.Design of Oligonucleotide Primers rpo105, rpo273, KY290  
and KY292 Showing High Specificity for MTB

Oligonucleotide primers specific for MTB (rpo105/rpo273 and  
5 KY290/KY292) (Table 2) were designed by making the 3' end complement  
and terminate at one of the newly identified unique positions (in the case of  
the upstream primers rpo105 and KY290, the 3' end is at site 130; in the  
case of downstream primer rpo273, it is at site 273, and in the case of  
10 downstream primer KY292, it is at position 282) (Figure 3). The remaining  
composition of the primers was based on direct complementarity to the MTB  
rpoB sequence, and the optimum length was determined with the aid of  
computer-generated thermal profiles (OLIGO Primer Analysis Software  
version 4.0 for the Macintosh, National Biosciences, Inc. Plymouth, MN).

15

Example 5.PCR using Primers KY290 and KY292

PCR using primer pair KY290/KY292 was conducted using  
target DNA from several mycobacterial reference strains. Strains *M.*  
20 *scrofulaceum* (ATCC# 19981), *M. smegmatis* (ATCC# 14468), *M. simiae*  
(ATCC# 25275), *M. xenopi* (ATCC# 19250), *M. brunense* (ATCC# 23434)  
and *M. chelonae* (ATCC# 35752) were obtained from the American Type  
Culture Collection. The other isolates were gifts from collaborator  
laboratories in Europe and identified in those laboratories. Isolation and  
25 purification of bacterial DNA was performed according to standard  
methodology. A general method for the isolation of mycobacterial DNA can  
be found in Patel et al., Journal of General Microbiology, 132, 541-551  
(1986). Oligonucleotide primers were synthesized using standard  
methodology. Methods of preparing oligonucleotides of specific sequence  
30 are known in the art, and include, for example, cloning and restriction of  
appropriate sequences, and direct chemical synthesis by a method such as  
the phosphotriester method of Narange et al., Meth. Enzymol., 68, 90-99  
(1979); the phosphodiester method of Brown et al., Meth. Enzymol., 68,  
109-151 (1979); the diethylphosphoramidite method of Beaucage et al.,  
35 Tetrahedron Lett., 22, 1859-1862 (1981); and the solid support method of

U.S. Patent No. 4,458,066, each incorporated herein by reference. A review of synthesis methods is provided in Goodchild, Bioconjugate Chemistry, 1, 165-187 (1990), incorporated herein by reference.

Primer pairs analyzed were rpo95/KY292 and KY290/KY292.

- 5 PCR reactions (100  $\mu$ l) contained target bacterial DNA (5  $\mu$ l), 50 mM Tris-HCl, pH 8.9, 50 mM KCl, 10% glycerol (Sigma Chemical Company, St. Louis, MO), 500 nM each primer, 2 mM  $MgCl_2$  (Perkin-Elmer-Cetus, Norwalk, CT), 0.2 mM each deoxyadenosine triphosphate (dATP), deoxyguanine triphosphate (dGTP), deoxycytidine triphosphate (dCTP) and
- 10 deoxythymidine triphosphate (dTTP) (i.e. dNTP, where "N" refers to A, G, C or T, (Perkin-Elmer-Cetus)), 3 units Taq polymerase (Perkin-Elmer-Cetus), and 1 unit uracil-N-glycosylase (Perkin-Elmer-Cetus). Thermal cycling was performed using a GeneAmp PCR System 9600 (Perkin-Elmer-Cetus). Conditions for amplification comprised an initial 50°C incubation for 2 min,
- 15 followed by 2 cycles of [98°C (20 sec), 62°C (20 sec) 72°C (45 sec)] and 35 cycles of [94°C (20 sec), 62°C (20 sec) 72°C (45 sec)], followed by a final 72°C incubation for at least 10 min for strand extension. Amplification products were analyzed by gel electrophoresis on 2% Nusiev/0.5% agarose gels (FMC Products, Rockland, ME) in a Tris-Borate-EDTA buffer
- 20 (composed as described in Sambrook et al., Molecular Cloning Manual) (incorporated herein by reference) and stained with ethidium bromide.

Primer pair KY290/KY292 amplified only *M. tuberculosis* and *M. chelonae*, whereas primer pair rpo95/KY292 amplified *M. kansasii* as well. Both pairs were highly sensitive, amplifying MTB DNA at the 100 fg

25 level.

TABLE 6		
Specificity of primer pairs rpo95/KY292 and KY290/KY292 <sup>1</sup>		
Mycobacterial species tested	rpo95/KY292	KY290/K6292
<i>M. tuberculosis</i>	+	+
<i>M. scrofulaceum</i>	-	-
<i>M. fortuitum</i>	-	-
<i>M. avium</i>	-	-
<i>M. kansasii</i>	+	-
<i>M. intracellulare</i>	-	-
<i>M. phlei</i>	-	-
<i>M. smegmatis</i>	-	-
<i>M. marinum</i>	-	-
<i>M. flavescens</i>	-	-
<i>M. xenopi</i>	-	-
<i>M. simiae</i>	-	-
<i>M. brunense</i>	-	-
<i>M. chelonae</i>	+	+

<sup>1</sup>A "+" entry indicates amplification, a "-" entry indicates no amplification.

5

#### Example 6.

#### PCR using MTB-specific Primers rpo105 and rpo273

#### in Combination with Less Specific Primers

Degenerate primers DDIDH, NMQRQ(#2) and FENLFF (Table 2) were designed with reference to highly conserved amino acid sequences in the bacterial *rpoB* gene as described in Example 2 for DDIDHL and NMQRQ(#1) (Figure 1). Like DDIDHL and NMQRQ(#1) they contained restriction sites to facilitate later cloning, if desired, as further described in the footnotes to Table 2. Primers rpo95, rpo105, rpo273, rpo293 and rpo397 were designed as described above in Example 2 and Example 4.

10

A. Bacterial DNA isolation. DNA from pure cultures of bacteria were prepared for polymerase chain reaction (PCR) amplification by one of the following methods:

5        Method BB/B. A 10- $\mu$ L loopful of each isolate was placed in a 2.0-ml screw cap microcentrifuge tube (Sarsted, Inc.) that contained 1.0 ml of 1XTE (1X TE: 10 mM Tris(hydroxymethyl)aminomethane hydrochloride (Tris-HCl), pH 8.0, 1 mM ethylenediaminetetraacetic acid (EDTA), 100X concentrate purchased from Sigma Chemical Company, St. Louis, MO), 1% Triton-X100 (Sigma), and filled 2/3 full with 0.1 mm diameter zirconium beads (BioSpec Products, Bartlesville, OK 74005). Tubes were oscillated on a MiniBeadBeater mechanical disrupter Model 3110 (BioSpec Products, Bartlesville, OK) for 30 seconds. The supernatant was pipetted into a clean tube, 10 boiled 30 minutes to kill the bacteria, and stored at -20°C until 15 needed. Two  $\mu$ L was used in a 50- $\mu$ L PCR.

20        Method BB/P. A 10- $\mu$ L loopful of each isolate was placed in a 0.5 ml screw cap microcentrifuge tube that contained 0.3 ml of TE-equilibrated phenol (phenol from Boehringer Mannheim Biochemicals, Inc., Indianapolis, IN), 150  $\mu$ l 1xTE, and was filled 2/3 full with 0.1-mm diameter zirconium beads. The mixture was oscillated 30 seconds on a Mini Bead Beater. The tubes were allowed to sit at room temperature for 15-30 minutes to kill the 25 bacteria, then centrifuged for 20 seconds in a microcentrifuge to separate phases. The aqueous phase was transferred to a new tube and stored at -20°C until needed. Since these samples contained phenol (phenol is somewhat soluble in the aqueous phase), the DNA from these samples was extracted using either the IsoQuick nucleic acid extraction kit (MicroProbe, Garden Grove, CA 92641) or the 30 Magic (now Wizard) DNA Cleanup kit (Promega Corp., Madison WI). The resultant DNA extract from either procedure was suspended in 50  $\mu$ l of water. Five  $\mu$ L of 1/10 or 1/100 dilutions of purified DNA in water was used as target for the PCR.

35

B. DNA extraction from clinical specimens. Clinical specimens (respiratory: sputum, induced sputum, bronchial wash/lavage; non-respiratory: gastric wash, urine, ankle tissue, groin tissue) were processed by 1% NaOH liquefaction-decontamination and sedimentation (Mayo Clinic Mycology and Mycobacteriology Clinical Laboratory Manual). The specimen that was leftover from standard clinical laboratory procedures was used for PCR analysis. the DNA was extracted from clinical specimens using one of the following methods:

10        Method L6/PBB. 200  $\mu$ l of residual specimen was placed in a 1.5 or 2.0 ml screw cap tube and centrifuged for 10 minutes at 14,000 x g. The supernatant was removed and the pellet suspended in 200  $\mu$ l of L6 buffer (5M guanidinium thiocyanate), 1% Triton X-100, 50 mM Tris-HCl (pH 6.4), 20 mM EDTA) (Boom et al., J. Clin. Microbiol., 15        1990). This material was transferred to a new 2 ml screw cap tube containing 750  $\mu$ l phenol-chloroform-isoamyl alcohol (25:24:1) and 2/3 full of 0.1 mm zirconium beads. The tube was shaken in a MiniBeadBeater for 2 minutes. The tube was allowed to rest for 15 min to assure killing of unlysed organisms, then centrifuged for 2 min to separate phases and pellet debris. the top aqueous phase was transferred to a new 1.5 ml snap top tube and subjected to IsoQuick kit DNA extraction method with the following modification. At the point the DNA is to be precipitated, 1  $\mu$ l of glycogen suspension (Boehringer Mannheim Biochemicals, Indianapolis, IN) was added to 25        promote the precipitation of DNA. This step was essential because of the wide variety of DNA concentrations present in these extracts. The resultant DNA pellet was suspended in 20  $\mu$ l of water and stored at -20°C until needed. Two  $\mu$ l of extracted material, or 2  $\mu$ l of a 1/10 dilution of the extract in water, was used in the nested PCR procedure described below.

30        Method P/BB-2. 1.0 ml of residual specimen was placed in a 2.0 ml screw cap tube and centrifuged for 15 minutes at 14,000 x g. The supernatant was removed, and the following were added to the tube: 35        600  $\mu$ l TE equilibrated phenol, 400  $\mu$ l 1X TE buffer, and 0.1 mm

diameter zirconium beads (2/3 full). The tube was then oscillated for 30 seconds using the MiniBeadBeater, incubated at room temperature for 15 min to kill the unlysed organisms, and centrifuged for 3 min at 12,000 x g to separate phases. The aqueous phase was transferred to a clean tube and stored at -20°C until needed. The DNA from the aqueous phase was extracted using the IsoQuick kit. Five µM of a 1/10 or 1/100 dilution of extracted DNA in water was used for the PCR.

C. Polymerase chain reactions. Oligonucleotide primers DDIDH, NMQRQ(#2), FENLFF, rpo95, rpo105, rpo273, and rpo293 (Table 2) were synthesized using an Applied Biosystems Model 394 Synthesizer (Applied Biosystems, Foster City, CA) and standard phosphoramidite chemistry (described in more detail in Example 5). The buffer and components (master mixes) used for PCR were as follows:

Master Mix I: This was the mix used for all non-nested PCRs and for the initial round of the hemi-nested PCRs described below. 5 µl target DNA was used per 50 µl PCR.

10 mM Tris-HCl, pH 8.3  
50 mM KCl  
10% glycerol  
1.5 mM MgCl<sub>2</sub>  
0.2 mM deoxyadenosine triphosphate (dATP)  
0.2 mM deoxyguanine triphosphate (dGTP)  
0.2 mM deoxycytidine triphosphate (dCTP)  
0.2 mM deoxyuridine triphosphate (dUTP)  
(all nucleoside triphosphates (dNTPs)  
from Boehringer Mannheim Biochemicals,  
Indianapolis, IN)  
0.125 µl/25 µl reaction AmpliTaq polymerase (5 units/µl,  
Perkin Elmer Cetus, Norwalk, CT).  
1 µM of each primer

Master Mix II: 75 µl of this master mix was added to a 25 µl PCR containing the components of Master Mix I. The final concentrations were the molar amounts present in the 75 µl volume that was added:

5

10 mM Tris-HCl, pH 8.3  
50 mM KCl  
10% glycerol  
1.5 mM MgCl<sub>2</sub>  
0.25 mM of each dNTP (see Master Mix I)  
2.5 units AmpliTaq polymerase  
1.25  $\mu$ M of each primer

10

Lysis and DNA extraction were done at one location, preparation of the PCR master mix at another, and amplification and amplicon analysis at a third to minimize the chance of contamination. In addition, the incorporation of dUTP facilitated elimination of any potentially contaminating amplified product. Either a Temptronic Series 669 (Barnstead-Thermolyne, Dubuque, IA 52004) or Perkin-Elmer Cetus Model 9600 thermal cycler was used.

15 Standard (non-nested) PCRs were carried out using the conditions described in Table 7. Hemi-nested PCRs make use of one upstream primer and two different downstream primers in two successive  
20 PCRs in order to provide greater sensitivity. Hemi-nested PCRs utilizing rpo105/rpo293 followed by rpo105/rpo273 were carried out in a single tube protocol. For the hemi-nested procedure an Ampliwax bead (Perkin Elmer Cetus, Norwalk, CT) was included in the first PCR reaction to act as a barrier to prevent inadvertant dilution and amplicon contamination of the  
25 work area. The first PCR employed rpo105/rpo293 as primers in a 25  $\mu$ l reaction. Conditions for amplification are described in Table 7. Upon completion of this PCR, 75  $\mu$ l of Master Mix II, containing primers rpo105/rpo273, was added to each tube (above the solidified Ampliwax layer). The tubes were then returned to the thermocycler. Conditions for  
30 the second round of amplification are also described in Table 7.

Table 7.PCR Cycling Parameters\*

5	<u>Primer Combinations</u>	<u>Temperature/Time</u>
	rpo95/rpo397	94°C/60 sec; 65°C/60 sec (50 cycles) alternative method 94°C/30 sec; 71°C/60 sec (50 cycles)
10	rpo95/rpo293	94°C/60 sec; 65°C/60 sec (50 cycles)
	rpo95/NMQRQ	94°C/30 sec; 61°C/60 sec; 72°C/60 sec (2 cycles) then 94°C/30 sec; 70°C/60 sec (50 cycles)
15	FENLFF/NMQRQ	94°C/30 sec; 61°C/60 sec; 72°C/60 sec (2 cycles) then 94°C/30 sec; 65°C/60 sec (50 cycles)
20	DIDDH/NMQRQ	94°C/30 sec; 61°C/60 sec; 72°C/60 sec (2 cycles) then 94°C/30 sec; 70°C/60 sec (50 cycles)
25	Single tube nested:	
	rpo105/rpo293	94°C/30 sec; 72°C/60 sec (25 cycles) then
	rpo105/rpo273	94°C/30 sec; 74°C/60 sec (50 cycles)

30

Amplification products were detected by agarose gel electrophoresis of 1/5 or 1/10 of the reaction mixture in 2% agarose (Seakem GTG, FMC, Rockland, ME 04841) made up in 1X Tris-borate-EDTA (TBE) (0.089M Tris-borate, 0.089M boric acid, 2mM EDTA), followed by staining with ethidium bromide. The products were purified by using Magic PCR Prep kit reagents (Promega, Madison, WI 53711), and sequenced by using primer rpo95 at the Mayo Clinic Molecular Biology Core Facility using an Applied Biosystems 373A automated sequencer and the dye-coupled dideoxyribonucleotide cycle sequencing method (Applied Biosystems, Inc., Foster City, CA). Sequencing reactions were run using 5% (v/v) dimethylsulfoxide for twenty-five cycles of 96°C (30 seconds), 50°C

35

40





TABLE 8

Specificity Challenge with Mycobacteria and Other G-C Rich Organisms

Primer set rpo105/rpo293/rpo273 in a Hemi-nested PCR

- |    |                                |
|----|--------------------------------|
| 5  | <u>Mycobacteria</u>            |
|    | <i>M. asiaticum</i>            |
|    | <i>M. avium-intracellulare</i> |
|    | <i>M. bordonii</i>             |
|    | <i>M. chelonae</i>             |
| 10 | <i>M. fortuitum</i>            |
|    | <i>M. gordonae</i>             |
|    | <i>M. kansasii</i>             |
|    | <i>M. malmoense</i>            |
|    | <i>M. marinum</i>              |
| 15 | <i>M. nonchromogenicum</i>     |
|    | <i>M. phlei</i>                |
|    | <i>M. scrofulaceum</i>         |
|    | <i>M. simiae</i>               |
|    | <i>M. smegmatis</i>            |
| 20 | <i>M. szulgai</i>              |
|    | <i>M. triviale</i>             |
|    | <i>M. tuberculosis</i>         |
|    | <i>M. xenopi</i>               |
| 25 | <u>Other G-C Rich Genera</u>   |
|    | <i>Actinomyces</i> sp.         |
|    | Aerobic Actinomycetes          |
|    | <i>Corynebacterium</i> sp.     |
|    | <i>Nocardia</i> sp.            |
| 30 | <i>Probionibacterium</i> sp.   |
|    | <i>Rhodococcus</i> sp.         |

TABLE 9

**Direct Detection of *M. tuberculosis* *rpoB* in  
53 Clinical Specimen Panel**

Specimen Source (n)	Results			
	<i>rpoB</i> <sup>1</sup>	IS6110 <sup>2</sup>	Smear <sup>3</sup>	Culture
Respiratory <sup>4</sup> (8)	+	+	+	MTB
Respiratory (11)	+	+	--	MTB
Respiratory (1)	+	--	--	MTB
Respiratory (2)	--	--	--	MTB
Respiratory (6)	--	--	--	--
Respiratory (3)	--	--	+	MOTT <sup>5</sup>
Respiratory (12)	--	--	--	MOTT
Respiratory (2)	--	+ <sup>6</sup>	--	MOTT
Respiratory (1)	+ <sup>7</sup>	--	--	MOTT
Respiratory (1)	+ <sup>7</sup>	--	+	MOTT
Respiratory (1)	+ <sup>7</sup>	--	--	--
Non-respiratory <sup>8-GW</sup> (1)	+	+	--	MTB
Non-respiratory <sup>8-U</sup> (1)	--	--	--	MTB
Non-respiratory <sup>8-A</sup> (1)	--	--	+	--
Non-respiratory <sup>8-G,GW</sup> (2)	--	--	--	MOTT

<sup>1</sup> Hemi-nested PCR using primer set *rpo105/rpo293/rpo273*.

<sup>2</sup> In vitro laboratory detection using IS6110.

<sup>3</sup> In vitro laboratory detection using acid fast smear.

<sup>4</sup> Includes sputum, induced sputum, bronchial wash/lavage.

<sup>5</sup> *Mycobacteria* other than *M. tuberculosis* (MOTT).

<sup>6</sup> False positive.

<sup>7</sup> Amplicon sequenced as TB; Repeat *rpoB* PCR was negative.

<sup>8</sup> GW: gastric wash; U: urine; A: ankle; G: groin.

All documents cited herein are incorporated by reference. The foregoing detailed descriptions and examples have been given for clarity of understanding only. No unnecessary limitations are to be understood therefrom. The invention is not limited to the exact details shown and described, for variations obvious to one skilled in the art will be included within the invention defined by the claims.

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANTS: Mayo Foundation for Medical Education and Research  
and Hoffmann-La Roche Inc.
- (ii) TITLE OF INVENTION: Detection of a Genetic Locus Encoding  
Resistance to Rifampin
- (iii) NUMBER OF SEQUENCES: 15
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Schwegman, Lundberg & Woessner
  - (B) STREET: 3500 IDS Center
  - (C) CITY: Minneapolis
  - (D) STATE: MN
  - (E) COUNTRY: USA
  - (F) ZIP: 55402
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: Unknown
  - (B) FILING DATE: 26-MAY-1995
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Raasch, Kevin W.
  - (B) REGISTRATION NUMBER: 35,651
  - (C) REFERENCE/DOCKET NUMBER: 150.105WO1
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 612-339-0331
  - (B) TELEFAX: 612-339-3061

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 970 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAGACGCTGT TGGAAACTT GTTCTTCAAG GAGAAGCGCT ACGACCTGGC CCGCGTCGGT	60
CGCTATAAGG TCAACAAGAA GCTCGGGCTG CATGTCGGCG AGCCCATCAC GTCGTCGACG	120
CTGACCGAAG AAGACGTGCT GGCCACCATC GAATATCTGG TCCGCTTGCA CGAGGGTCAG	180
ACCACGATGA CGGTTCCGGG CGGCGTCGAG GTGCCGGTGG AAACCGACGA CATCGACCAC	240
TTCGGCAACC GCCGCCTGCG TACGGTCGGC GAGCTGATCC AAAACCAGAT CCGGGTCGGC	300
ATGTCGCGGA TGGAGCGGGT GGTCCGGGAG CGGATGACCA CCCAGGACGT GGAGGCGATC	360
ACACCGCAGA CGTTGATCAA CATCCGGCCG GTGGTCGCGG CGATCAAGGA GTTCTTCGGC	420
ACCAGCCAGC TGAGCCAATT CATGGACCAG AACAAACCGC TGTCCGGGGT GACCCACAAG	480
CGCCGACTGT CGGCGCTGGG GCCCGGCGGT CTGTCACGTG AGCGTGCCGG GCTGGAGGAG	540
CGCGACGTGC ACCCGTCGCA CTACGGCCGG ATGTGCCCGA TCGAAACCCC TGAGGGGCCC	600
AACATCGGTC TGATCGGCTC GCTGTGGTG TACGCGCGGG TCAACCGTT CGGGTTCATC	660
GAAACGCCGT ACCGCAAGGT GGTGACGGC GTGGTTAGCG ACGAGATCGT GTACCTGACC	720
GCCGACGAGG AGGACCGCCA CGTGGTGGCA CAGGCCAATT CGCCGATCGA TGCGGACGGT	780
CGCTTCGTG AGCCGCGCGT GCTGGTCCG CGCAAGGCGG GCGAGGTGGA GTACGTGCC	840
TGCTCTGAGG TGGACTACAT GGACGTCTG CCCCGCCAGA TGGTGTCCGT GGCCACCGCG	900
ATGATTCCCT TCCTGGAGCA CGACGACGCC AACCGTGCCC TCATGGGGGC AAACATGCAG	960
CGCCAGGCGG	970

## (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TTGAATTCGA YGAYATHGAY CAYCT

25

## (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTCCCTGCAG GACGACATCG ACCAC

25

## (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTGGATCCYT GVCYTG CAT RTT

23

## (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGGATCCGCGY TCCGYTG CAT GTT

23

## (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCCTGCAGTT CGAGAACCTG TTCTTC

26

## (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCACCCAGGA CGTGGAGGCG ATCACAC

27



## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AGTGGACGCG GTGCACGTCG CGGACCT

27

## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGTTTCGATG AACCCGAACG GGTTCAC

27

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGTGGAGGCG ATCACACCGC AGACGT

26

## (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GACCTCCAGC CCGGCACGCT CACGT

25

## (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGCGATCACA CCGCAGACGT

20

## (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGACCTCCAG CCCGGCA

17

## (2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Asp Asp Ile Asp His Leu  
1 5

## (2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Asn Met Gln Arg Gln  
1 5

## WHAT IS CLAIMED IS:

1. A method for detecting *M. tuberculosis* or mutants thereof in a biological sample comprising:
  - (a) isolating DNA from the biological sample;
  - (b) amplifying the isolated DNA under hybridizing conditions with a primer set that targets portions of the gene encoding *rpoB*; wherein the primer set comprises at least one primer that hybridizes under hybridizing conditions to a nucleotide sequence containing at least one signature nucleotide for *M. tuberculosis*; and
  - (c) isolating and analyzing the amplified DNA to determine the presence or absence of *M. tuberculosis* or mutants thereof.
2. The method of claim 1 wherein the biological sample is a fluid or tissue sample from a human patient.
3. The method of claim 1 wherein the *M. tuberculosis* is resistant to rifampin.
4. The method of claim 3 wherein the *M. tuberculosis* is resistant to rifampin and at least one other antibiotic.
5. The method of claim 1 wherein the signature nucleotide is contained within 5 nucleotides of the 3' end of the primer.
6. The method of claim 5 wherein the signature nucleotide is the last nucleotide at the 3' end of the primer.
7. The method of claim 6 wherein the primer substantially corresponds to a primer selected from the group consisting of *rpo105*, *rpo273*, KY290 and KY292.

8. The method of claim 7 wherein the primer is *rpo105* or *rpo273*.
9. The method of claim 1 wherein the primer set further includes at least one primer substantially corresponding to a primer selected from the group consisting of *rpo95*, *rpo293* and *rpo397*.
10. A primer having 14-50 nucleotides, wherein the primer is derived from an AT-rich portion of the bacterial gene encoding *rpoB* that encodes a highly conserved amino acid sequence.
11. The primer of claim 10 that hybridizes under hybridizing conditions to nucleotides 1945-1980 in the *rpoB* gene shown in Figure 3.
12. The primer of claim 11 substantially corresponding to the hybridizing region on a primer represented by the degenerate nucleotide sequence designated FENLFF shown in Table 2.
13. The primer of claim 12 which is a primer represented by the degenerate nucleotide sequence designated FENLFF shown in Table 2.
14. The primer of claim 10 that hybridizes under hybridizing conditions to nucleotides 2160-2190 in the *rpoB* gene shown in Figure 3.
15. The primer of claim 14 substantially corresponding to primer DDIDH.
16. The primer of claim 15 which is primer DDIDH.
17. The primer of claim 14 substantially corresponding to the hybridizing region on a primer represented by the degenerate nucleotide sequence designated DDIDHL shown in Table 2.

18. The primer of claim 17 which is a primer represented by the degenerate nucleotide sequence designated DDIDHL shown in Table 2.
19. The primer of claim 10 that hybridizes under hybridizing conditions to nucleotides 2890-2910 in the *rpoB* gene shown in Figure 3.
20. The primer of claim 19 substantially corresponding to the hybridizing region on a primer represented by the degenerate nucleotide sequence designated NMQRQ(#) shown in Table 2.
21. The primer of claim 20 which is a primer represented by the degenerate nucleotide sequence designated NMQRQ(#1) shown in Table 2.
22. The primer of claim 19 substantially corresponding to the hybridizing region on a primer represented by the degenerate nucleotide sequence designated NMQRQ(#2) shown in Table 2.
23. The primer of claim 20 which is a primer represented by the degenerate nucleotide sequence designated NMQRQ(#2) shown in Table 2.
24. A primer that hybridizes under hybridizing conditions to a nucleotide sequence containing at least one signature nucleotide for *M. tuberculosis*.
25. The primer of claim 24 wherein the signature nucleotide hybridizes to the primer within 5 nucleotides of the 3' end of the primer.
26. The primer of claim 24 wherein the signature nucleotide hybridizes to the nucleotide at the 3' end of the primer.

27. The primer of claim 24 comprising 14-50 nucleotides.
28. The primer of claim 27 substantially corresponding to primer rpo105.
29. The primer of claim 28 which is primer rpo105.
30. The primer of claim 27 substantially corresponding to primer rpo273.
31. The primer of claim 30 which is primer rpo273.
32. The primer of claim 27 substantially corresponding to primer KY290.
33. The primer of claim 32 which is primer KY290.
34. The primer of claim 27 substantially corresponding to primer KY292.
35. The primer of claim 34 which is primer KY292.
36. A primer substantially corresponding to primer rpo95.
37. The primer of claim 36 which is primer rpo95.
38. A primer substantially corresponding to primer rpo293.
39. The primer of claim 38 which is primer rpo293.
40. A primer substantially corresponding to primer rpo397.
41. The primer of claim 40 which is primer rpo397.

## FIGURE 1

A PARTIAL AMINO ACID SEQUENCE ALIGNMENT OF THE *rpoB* GENE Product

	400									450
M. leprae	l	k		s	q		k	k	ar	y v kk
M. tuberculosis	l	k		s	q		k	k	ar	y v kk
E. coli				r	s				a	s l..
S. typhimurium				r	s				a	s l..
P. putida						n	a		pl	ri ..
Consensus	LVEIYRMRP	GEPPTKEAAE	TL	<del>LEN</del>	<del>EE</del> FESE	DRYDLS-VGR	MKFNR-LGLH			
	451									500
M. leprae	ag	lit	st	te	atie	y	rlhe	qs		t
M. tuberculosis	vg	pit	st	te	atie	y	rlhe	qt		t
E. coli	e					k				
S. typhimurium	d					k				
P. putida	t					t				
Consensus	R-EIEGSGIL	SKEDIVDMK	-LVDIRNGKG	TMTVPGGVEV	PVEVDDIDHL					
	501									550
M. leprae	l	t	iq	i	s	m	v	r	ttq	v ait t ir
M. tuberculosis	l	t	iq	i	s	m	v	r	ttq	v ait t ir
E. coli	s								g l t	
S. typhimurium	s								g l t	
P. putida	c								a s g	
Consensus	GNRRIR-VGE	MAENQFRVGL	VRVERAVKER	LSL-D-E-LM	PQDLINAKPV					
	551									600
M. leprae	v		t			gl		l	s	
M. tuberculosis	v		t			gl		l	s	
E. coli	s			v				i		
S. typhimurium	s							i		l
P. putida	a							c		
Consensus	-AAVKEFFGS	SQLSQFMDQN	NPLSEITHKR	R-SALGPGGL	TRERAGFEVR					
	601									650
M. leprae	s	m				g		v	p	i
M. tuberculosis	s	m				g		v	p	i
E. coli								q	e	t
S. typhimurium								q	e	r
P. putida						aa		q		s v k
Consensus	DVHPHYGRV	CPIETPEGPN	IGLINSLSVY	ARTN-YGFLE	TPYRKVV DGV					
	651									700
M. leprae	e	t	d	dr		pi	a	r	sssracw	r veyvas
M. tuberculosis	v	t	d	dr		pi	a	r	pr l r	veyvps
E. coli	t	h		gny		n		h	c s	sslfsr
S. typhimurium	t	h		gny		n		h	c s	sslfsr
P. putida	v			ad		saa	n	kkq	a h l.n	ftvkap
Consensus	VSDEI-YLSA	IEE--HVIAQ	ANS-LD-EG-	FVEDLVTVR-	KAGE-----					
	701									750
M. leprae	s		r	m	ta					lv s r
M. tuberculosis	s		r	m	ta					lv s a
E. coli	q		t	q	g					
S. typhimurium	q		t	q	g					
P. putida	tl			k						
Consensus	DEV DYM D VSP	-QVVSVAASL	IPFLEHDDAN	RALMGANMOR	QAVPTLRADK					



	91								
M. nonchromo	t	n	c	g	a	g	g-	*	* *
M. fortuitum	n	t	c	c	g	a	g	g	g
M. fortuitum	n	t	c	c	g	a	g	g	g
M. fortuitum	n	n	c	c	g	a	g	g	g
M. chelonae	nn	t	nt	c	c	a	g	g	g
M. xenopi	n	t	c	c	g				
M. kansasii	n								
M. avium-inter	gc ag	n	c	c	g				
M. avium-inter	gc ag			c					
M. avium-inter	ngc ag		t	a	c	g	ag		
M. avium-inter	ggc ag		c						
M. avium-inter	a		c	a	c				
M. bovis	n	gt							
M. tuberculosis	n	gt n n	n	n n n	n	n	ag	a	n
M. tuberculosis	gt						ag	a	n
M. tuberculosis	gt						ag	a	n
M. tuberculosis	gt						ag ta	a	n
Telente Genbank L05910	COG CAG ACC ATC AAC ATC CGG GGC GTG GCC GCG ATC AAG GAG TTC TTC GGC ACC AGC CAG CTG TCC CAG TTC ATG GAC CAG AAC								
Aerobic actino	n	gt	t	c c g gg t	n	n	c ag	cn	
A. viscosus	. a c c			acg n			c ag		
N. brasiliensis	n	n	c	ng nt	n	n	tc	atg	g
N. brasiliensis	n	c	c	ng nt	n	a	tc	atg	g
N. otitis	c n n g	c c c g ng t	c	n c cn n tcg	n	n	tcg	n	t
Rhodococcus	n tg	n	n	g	g		tcg	g	cg
Rhodococcus	gtc tg n ac	t nc n ct	tc gc ccg nn ng	n	nn n	ag ngg cag g	g t c a . . .		
Corynebacterium	c n c c	n g g g tc	c t t g c	cnc a	n n c tc	n c a a	n	a	nnn
Corynebacterium	ant t t t	t g	c tct t t	t cgc a	t t t tc			t	
Corynebacterium	n g c	c	c	n	n	a	tcg	g	t
Propionibacter	n n c	c	acg nt n	n	n	tc	c g	g	
Propionibacter	nn	n c	acg t	acg t		tc	c g	g	

M. nonchromo  
M. fortuitum  
M. fortuitum  
M. fortuitum  
M. chelonae  
M. chelonae  
M. xenopi  
M. kansasii  
M. avium-inter  
M. avium-inter  
M. avium-inter  
M. avium-inter  
M. avium-inter  
M. avium-inter  
M. bovis  
M. tuberculosis  
M. tuberculosis  
M. tuberculosis  
M. tuberculosis  
elente Genbank L0

Conse  
Aerobic actino  
A. bovis  
A. viscosus  
N. brasiliensis  
N. brasiliensis  
N. otitis  
Rhodococcus  
Rhodococcus  
Corynebacterium  
Corynebacterium  
Corynebacterium  
Propionibacter  
Propionibacter

Telente Genbank L05910

## Consensus

## Aerobic actino

**A. bovis**

**A. viscosus**

**N. brasiliensis**

**N. brasiliensis**

**N. otitis**

## Rhodococcus

## Rhodococcus

**Corynebacterium**

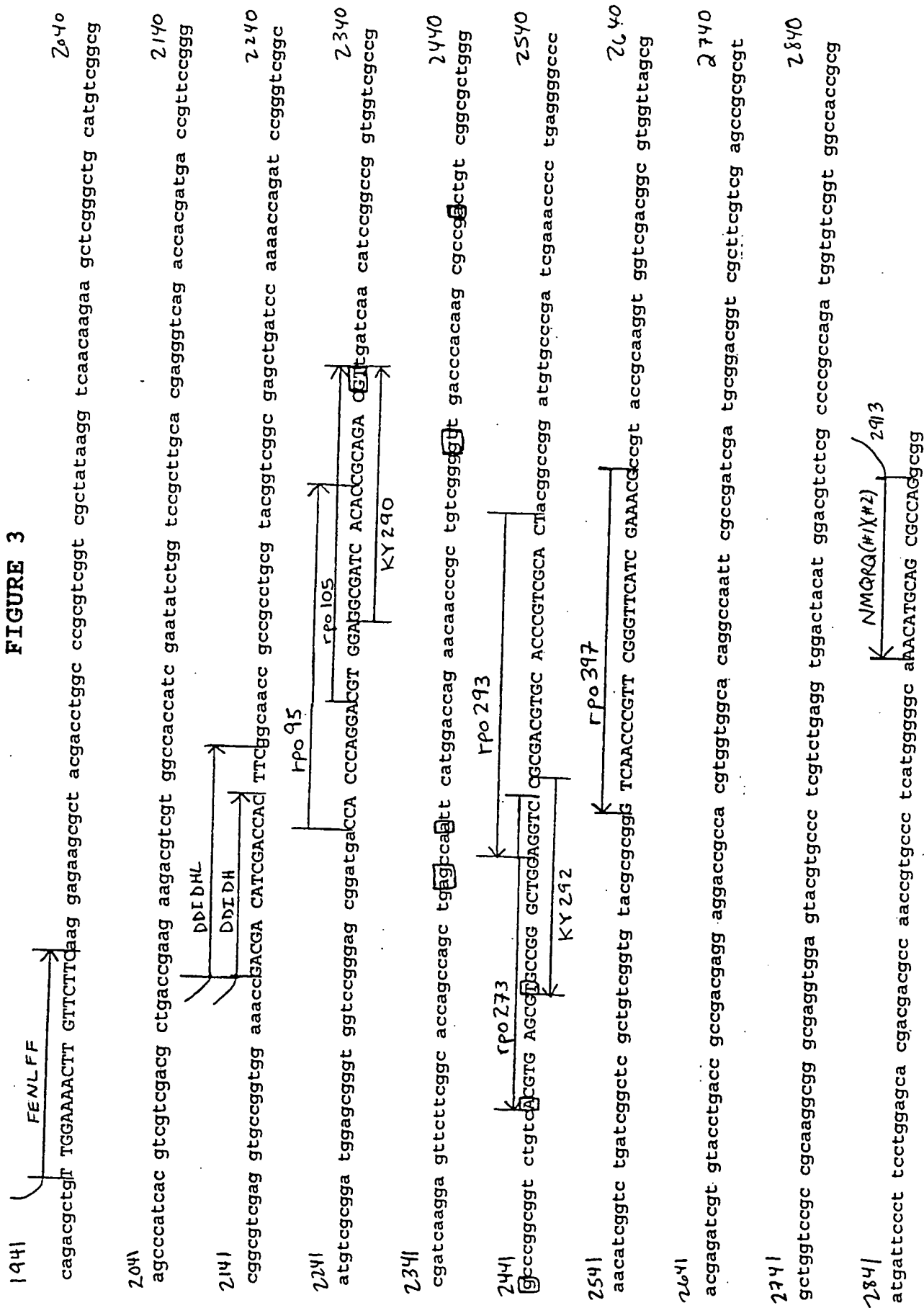
**Corynebacterium**

**orynebacterium**

**propionibacter**

**copriobacter**

FIGURE 3



## INTERNATIONAL SEARCH REPORT

Internal Application No  
PCT/US 95/06790A. CLASSIFICATION OF SUBJECT MATTER  
IPC 6 C12Q1/68 C07H21/04 C12P19/34

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)  
IPC 6 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DISEASE MICROBIOLOGY AND INFECTIOUS DISEASE, vol. 16, no. 4, April 1994 pages 219-227, HUNT, J. ET AL. 'detection of a genetic locus encoding resistance to rifampin in mycobacterial cultures and in clinical specimens' see the whole document	1-41
X	ABST. GEN MEET. AM. SOC. MICROBIOL., vol. 94, no. 0, 23 May 1994 page 196 WHELEN, A. ET AL. 'rapid and specific PCR-based detection of drug-resistant and -sensitive Mycobacterium tuberculosis' see abstract u-134	1-41

☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

## \* Special categories of cited documents:

- \*A\* document defining the general state of the art which is not considered to be of particular relevance
- \*E\* earlier document but published on or after the international filing date
- \*L\* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- \*O\* document referring to an oral disclosure, use, exhibition or other means
- \*P\* document published prior to the international filing date but later than the priority date claimed

- \*T\* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- \*X\* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- \*Y\* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- \* & \* document member of the same patent family

Date of the actual completion of the international search

15 September 1995

Date of mailing of the international search report

13.10.95

Name and mailing address of the ISA

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Authorized officer

Osborne, H

## INTERNATIONAL SEARCH REPORT

Internat'l Application No  
PCT/US 95/06790

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

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Y	EP,A,0 463 395 (F. HOFFMANN-LA ROCHE AG) 2 January 1992 see the whole document ---	1-41
A	WO,A,93 22454 (INSTITUT PASTEUR) 11 November 1993 see the whole document ---	1
A	ANTIMICROBIAL AGENTS AND CHEMOTHERAPY, vol. 37, no. 10, October 1993 pages 2054-58, TELENTI, A. ET AL. 'direct, automated detection of rifampin-resistance mycobacterium tuberculosis by polymerase chain reaction and single strand conformation polymorphism analysis' see the whole document -----	1

# INTERNATIONAL SEARCH REPORT

Information on patent family members

Internat'l Application No  
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